IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: da Costa e Silva, et al.
SERIAL NUMBER: 10/764,259   GROUP: 1638
FILING DATE: January 23, 2004   EXAMINER: Collins
TITLE: **PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE IN PLANTS**

Commissioner for Patents
PO Box 1450
Alexandria, VA 22313-1450

Sir:

DECLARATION PURSUANT TO 37 C.F.R. § 1.132

In support of the above-identified application, Ruoying Chen states the following:

1. I obtained my Bachelor of Science in Biophysics from Fudan University of China, and my Master of Science in Biochemistry from State University of New York at Binghamton in 1994. From 1994 to 2000, I was a biochemist/molecular biologist at Pioneer Hi-Bred International, Inc. From 2000 to 2005, I was a bioinformatician at BASF Plant Science L.L.C. I have more than ten years' experience in the field of Biology and more than five years' experience in the bioinformatics field. I am a coinventor in the above-identified application.

2. I have performed a protein sequence comparison using Vector NTI application (Invitrogen, 1600 Faraday Ave., Carlsbad, CA92008) at default settings between the *Physcomitrella patens* PP2A-4 protein disclosed as SEQ ID NO:13 in the above-identified application and the protein sequences of the five serine-threonine phosphatases set forth in Table 4 of the application, Q07098, Q07099, Q9MB05, Q9MB06, and Q9ZSE4. The results are shown in Exhibit 1 attached hereto.

3. The Prosite database (product of the Swiss Institute of Bioinformatics, http://www.isb-sib.ch/) search identifies the Serine/Threonine phosphatase motif as including the amino acids leucine-arginine-glycine-asparagine-histidine-glutamic acid, designated as LRGNHE in Exhibit 1.

All statements made herein of declarant's knowledge are true, and all statements made on declarant's information and belief are believed to be true. The statements made herein were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.
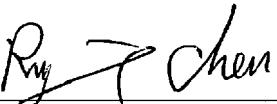
Date: _08/15/2006_

Ruoying Chen

Exhibit 1

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                       1                                        40
SEQ ID NO:13    (1)    MPSYADVDRQIEQLSECKPLSELEVKNLCDQARTILVEEW
      Q07098    (1)    MPSNGDLDRQIEQLMECKPLSEADVRTLCDQARAILVEEY
      Q07099    (1)    MPLNGDLDRQIEQLMECKPLGEADVKILCDQAKAILVEEY
      Q9MB05    (1)    MPSQADLDRQIEHLMECKPLTESEVKALCDQARAILVEEW
      Q9MB06    (1)    MPSHADLDRQIEHLMECKPLPEADVKALCDQARAILVEEW
      Q9ZSE4    (1)    MPSHGDLDRQIEHLMECKPLPEARGQTLCDQARAILVEEW
   Consensus    (1)    MPSNADLDRQIEQLMECKPLSEADVK LCDQARAILVEEW


                       41                                       80
SEQ ID NO:13    (41)   NVQPVKCPVTVCGDIHGQFHDLIELFRIGGKAPDTNYLFM
      Q07098    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGNAPDTNYLFM
      Q07099    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGNAPDTNYLFM
      Q9MB05    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGHAPHTNYLFM
      Q9MB06    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGNAPDTNYLFM
      Q9ZSE4    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGNAPDTNYLFM
   Consensus    (41)   NVQPVKCPVTVCGDIHGQFYDLIELFRIGGNAPDTNYLFM


                       81                                       120
SEQ ID NO:13    (81)   GDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI
      Q07098    (81)   GDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI
      Q07099    (81)   GDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI
      Q9MB05    (81)   GDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQI
      Q9MB06    (81)   GDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI
      Q9ZSE4    (81)   GDYVDRGYYSVETVTLLVALKVRYRDRITILRGNHESRQI
   Consensus    (81)   GDYVDRGYYSVETVSLLVALKVRYRDRITILRGNHESRQI


                       121                                      160
SEQ ID NO:13    (121)  TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIEHET
      Q07098    (121)  TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQV
      Q07099    (121)  TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQV
      Q9MB05    (121)  TQVYGFYDECLRKYGNANVWKEFTDLFDYLPLTALIESQV
      Q9MB06    (121)  TQVYGFYDECLRKYGNANVWKEFTDLFDYLPLTALIESQI
      Q9ZSE4    (121)  TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQI
   Consensus    (121)  TQVYGFYDECLRKYGNANVWKYFTDLFDYLPLTALIESQI


                       161                                      200
SEQ ID NO:13    (161)  FCLHGGLSPSLDTLDHIRALDRIQEVPHEGPMCDLLWSDP
      Q07098    (161)  FCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCDLLWSDP
      Q07099    (161)  FCLHGGLSPSLDTLDNIRSLDRIQEVPHEGPMCDLLWSDP
      Q9MB05    (161)  FCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCDLLWSDP
      Q9MB06    (161)  FCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCDLLWSDP
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Q9ZSE4      (161)  FCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCDLLWSDP
Consensus   (161)  FCLHGGLSPSLDTLDNIRALDRIQEVPHEGPMCDLLWSDP


                   201                                        240
SEQ ID NO:13 (201)  DDRCGWGISPRGAGYTFGQDIAEQFNHTNGLSLVARAHQL
Q07098      (201)  DDRCGWGISPRGAGYTFGQDIAAQFNHNNGLSLISRAHQL
Q07099      (201)  DDRCGWGISPRGAGYTFGQDIATQFNHNNGLSLISRAHQL
Q9MB05      (201)  DDRCGWGISPRGAGYTFGQDIASQFNHTNGLSLISRAHQL
Q9MB06      (201)  DDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQL
Q9ZSE4      (201)  DDRCGWGISPRGAGYTFGQDIAAQFNHTNGLTLISRAHQL
Consensus   (201)  DDRCGWGISPRGAGYTFGQDIAAQFNHTNGLSLISRAHQL


                   241                                        280
SEQ ID NO:13 (241)  VMEGYNWCQDKNVVTVFSAPNYCYRCGNMAAIMEIDETMN
Q07098      (241)  VMEGFNWCQDKNVVTVFSAPNYCYRCGNMAAILEIGENME
Q07099      (241)  VMEGYNWCQEKNVVTVFSAPNYCYRCGNMAAILEIGEKME
Q9MB05      (241)  VMEGYNWAQEKNVVTVFSAPNYCYRCGNMAAILEIGENMD
Q9MB06      (241)  VMEGYNWCQEKNVVTVFSAPNYCYRCGNMAAILEIGENMD
Q9ZSE4      (241)  VMEGYNWCQEKNVVTVFSAPNYCYRCGIMAAILEIGENMA
Consensus   (241)  VMEGYNWCQEKNVVTVFSAPNYCYRCGNMAAILEIGENMD


                   281                        307
SEQ ID NO:13 (281)  RSFLQFEPAPRQSEPDVTRKTPDYFL-
Q07098      (281)  QNFLQFDPAPRQVEPDTTRKTPDYFL-
Q07099      (281)  QNFLQFDPAPRQVEPDTTRKTPDYFL-
Q9MB05      (281)  QNFLQFDPAPRQIEPDTTRKTPDYFL-
Q9MB06      (281)  QNFLQFDPAPRQIEPDTTRKTPDYFL-
Q9ZSE4      (281)  QNFLQFDPAPRQIEPDTTRKTPDYFL-
Consensus   (281)  QNFLQFDPAPRQIEPDTTRKTPDYFL
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Note: The underlined area is the Serine/Threonine phosphatase motif (LRGNHE) identified using the Prosite database.